

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 13:11:32 ; Search time 3628.34 Seconds
(Without alignments)
11761.720 Million cell updates/sec

Title: US-09-784-340-1

Perfect score: 2759

Sequence: 1 caaccatgcagatcagtgct.....ctgtcagccgttactgtagcg 2759

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1344157 seqs, 773874588 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2688314

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl:*
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15	32	1.2	2075	88	AF072223	AF072223 Macaca fa
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ALIGNMENTS

RESULT 1
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 LOCUS Homo sapiens cDNA: FLJ21934 fis, clone HEP04364.
 DEFINITION AK025587.1 GI:10438147
 ACCESSION AK025587.1
 VERSION AK025587.1
 KEYWORDS oligo capping; fis (full insert sequence);
 Homo sapiens hepatoma cell_line:HepG2 cDNA to mRNA, clone_11b:HEP
 SOURCE clone:HEP04364.

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE

1 (sites)
 Kawabata,A., Hiki,T., Kobatake,N., Inagaki,H., Ikema,Y.,
 Okamoto,S., Okitani,R., Ota,T., Suzuki,Y., Obayashi,M., Nishi,T.,
 Shibahara,T., Tanaka,T., Nakamura,Y., Isogai,T. and Sugano,S.
 NEDO human cDNA sequencing project

TITLE

Unpublished (2000)
 2 (bases 1 to 2786)

JOURNAL

Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T.,
 Shibahara,T., Tanaka,T. and Nakamura,Y.
 Direct Submission

AUTHORS

Submitted (29-AUG-2000) to the DDBJ/EMBL/Genbank databases. Sumio
 Sugano, Institute of Medical Science, University of Tokyo,
 Laboratory of Genome Structure Analysis, Human Genome Center;
 Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
 (E-mail:cdna@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,
 Fax:81-3-5449-5416)

COMMENT

NEDO human cDNA sequencing project supported by Ministry of
 International Trade and Industry of Japan; cDNA full insert
 sequencing; Research Association for Biotechnology; cDNA library

construction, 5'- & 3'-end one pass sequencing; Department of
 Virology and Human Genome Center, Institute of Medical Science,
 University of Tokyo (partly supported by Science and Technology
 Agency).

FEATURES

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CDS

BASE COUNT 919 a 463 c 496 g 908 t
 ORIGIN

Query Match 54.4%; Score 1502; DB 89; Length 2786;
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OY	922	gaattcagggggaatgtagtatgtgtgttcttcctcggggtcaactggtt	981
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Db	901	ACCCCAAAATGATCTTCTTGGTCATCCCAAAACAAAGCTTTATAC	960
OY	1162	gaatgggactctgaagaacttatcaatcgggggtccctcctggtggagt	1221
Db	961	GAAATGGGATCTATGACCTATTTTACATGAGGGGTCCCTATGTGGG	1020
OY	1222	tgaatcagcttgataacataagctacacatgaaagccaaagagcagct	1281
Db	1021	TGATCAGCTTGATATACATATACCTCAATGAAGGCCAAAGAGCAG	1080
OY	1282	caaaactatgacaaagcgaagatttactcggaggttggaagaagtcata	1341
Db	1081	CAAAACATATGACCAAGCCAAATTTACTAGAGGGCTTTGAAACAGT	1140
OY	1342	ttataaagagaatctcctatgagattatcaagaatcacaatgataac	1401
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OY	1402	agatcgagcagctctctctgagattgtcatalcgcgccaaagagccaa	1461
Db	1201	AGATCGAGCGAGTCTTCTCGATGTCAGATGTTGTCATGCGCCCA	1260
OY	1462	atcagctgcacatgacctaccggtttccagacatactatagatgtagt	1521
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LOCUS	AC021146	212904 bp	DNA
DEFINITION	Homo sapiens chromosome 4 clone RP11-468N14, WORKING	HTG	07-JUL-2000
SEQUENCE	24 unordered pieces.		DRAFT
AC021146			
VERSION	AC021146.4	GI:8568861	

KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eumalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
AUTHORS	1 (bases 1 to 212904)
TITLE	Waterston, R.H.
JOURNAL	The sequence of Homo sapiens clone
REFERENCE	unpublished
AUTHORS	2 (bases 1 to 212904)
TITLE	Waterston, R.H.
JOURNAL	Direct Submission
COMMENT	Submitted (14-JAN-2000) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA
COMMENT	On Jun 16, 2000 this sequence version replaced gi:7344259.

HTG; HTGS_PHSSE1; HTGS_DRAFT.
human.
Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo
1 (bases 1 to 212904)
Waterson,R.H.
The sequence of Homo sapiens clone
unpublished
2 (bases 1 to 212904)
Waterson,R.H.
Direct Submission
Submitted (14-JAN-2000) Genome Sequencing Center, Washing
University School of Medicine, 4444 Forest Park Parkway, S
MO 63108, USA
On Jun 16, 2000 this sequence version replaced gi:7344259

----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Project Information
Center project name: H_NH0468N14
----- Summary Statistics -----
Sequencing vector: M13, 88%
Sequencing vector: plasmid, 12%
Chemistry: Dye-Primer ET; 88% of reads
Chemistry: Dye-Terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199729 bases at least Q40
Consensus quality: 203731 bases at least Q30
Consensus quality: 206340 bases at least Q20
Insert size: 213000; agarose-fp
Insert size: 210604; sum-of-ctrls
Quality coverage: 3.75 in Q20 bases; sum-of-ctrls
Quality coverage: 3.83 in Q20 bases; sum-of-ctrls

----- NOTE: This is a 'working draft' sequence. It currently
consists of 24 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.

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1565	1664:	gap of unknown length
1565	3085:	contig of 1421 bp in length
3086	3185:	gap of unknown length
3186	5134:	contig of 1949 bp in length
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5235	8169:	contig of 2935 bp in length
8170	8269:	gap of unknown length
8270	10341:	contig of 2072 bp in length
10342	10441:	gap of unknown length
10442	13614:	contig of 3173 bp in length
13615	13714:	gap of unknown length
13715	17089:	contig of 3375 bp in length
17090	17189:	gap of unknown length
17190	20701:	contig of 3512 bp in length
20702	20801:	gap of unknown length
20802	25001:	contig of 4200 bp in length
25002	25101:	gap of unknown length
25102	28020:	contig of 3919 bp in length
28021	29120:	gap of unknown length
29121	33356:	contig of 4236 bp in length
33357	33456:	gap of unknown length
33457	35902:	contig of 3446 bp in length
35903	37002:	gap of unknown length
37003	42975:	contig of 5973 bp in length
42976	43075:	gap of unknown length
43076	46839:	contig of 5264 bp in length
46839	48340:	gap of unknown length

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LOCUS	AC021146	212904 bp	DNA
DEFINITION	Homo sapiens chromosome 4 clone RP11-468N14, WORKING DRAFT	HTG	07-JUL-2000
ACCESSION	AC021146		
VERSION	AC021146.4	GI:8568861	
KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
TITLE	1 (bases 1 to 212904)		
JOURNAL	Waterston,R.H.		
REFERENCE	The sequence of Homo sapiens clone		
AUTHORS	Unpublished		
TITLE	2 (bases 1 to 212904)		
JOURNAL	Waterston,R.H.		
REFERENCE	Submitted (14-JAN-2000) Genome Sequencing Center, Washington		
AUTHORS	University School of Medicine, 4444 Forest Park Parkway, St. Louis		
TITLE	MO 63108, USA		
COMMENT	On Jun 16, 2000 this sequence version replaced gi:7344259.		

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----- Genome Center -----
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu/gsc/index.shtml
----- Project Information -----
Center project name: H.NH0468N14
----- Summary Statistics -----
Sequencing vector: M13; 888
Sequencing vector: plasmid; 128
Chemistry: Dye-primed ET; 888 of reads
Chemistry: Dye-terminator Big Dye; 12% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 199729 bases at least Q40
Consensus quality: 203731 bases at least Q30
Consensus quality: 206340 bases at least Q20
Insert size: 213000; agarose-fp
Insert size: 210604; sum-of-contigs
Quality coverage: 3.75 in Q20 bases; agarose-fp
Quality coverage: 3.83 in Q20 bases; sum-of-contigs
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 24 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
-----
1
1564: contig of 1564 bp in length
1565
1665: gap of unknown length
1665
3085: contig of 1421 bp in length
3086
3185: gap of unknown length
3186
5134: contig of 1949 bp in length
5135
5234: gap of unknown length
5235
8169: contig of 2935 bp in length
8170
8269: gap of unknown length
8270
10341: contig of 2072 bp in length
10342
10441: gap of unknown length
10442
13514: contig of 3173 bp in length

```

*	13615	13714:	gap of unknown length
*	13715	17089:	contig of 3375 bp in length
*	17090	17189:	gap of unknown length
*	17190	20701:	contig of 3512 bp in length
*	20702	20801:	gap of unknown length
*	20802	25001:	contig of 4200 bp in length
*	25002	25101:	gap of unknown length
*	25102	29020:	contig of 3919 bp in length
*	29021	29120:	gap of unknown length
*	29121	33356:	contig of 4236 bp in length
*	33357	33456:	gap of unknown length
*	33457	35902:	contig of 3446 bp in length
*	35903	37002:	gap of unknown length
*	37003	42975:	contig of 5973 bp in length
*	42976	43075:	gap of unknown length
*	43076	48339:	contig of 5264 bp in length
*	48340	48439:	gap of unknown length
*	48440	55529:	contig of 8090 bp in length
*	55529	56629:	gap of unknown length
*	56630	65213:	contig of 8584 bp in length
*	65214	65313:	gap of unknown length
*	65314	74715:	contig of 9402 bp in length
*	74716	74815:	gap of unknown length
*	74816	88546:	contig of 13731 bp in length
*	88547	88646:	gap of unknown length
*	88647	103367:	contig of 14721 bp in length
*	103368	103467:	gap of unknown length
*	103468	118167:	contig of 14700 bp in length
*	118168	118267:	gap of unknown length
*	118268	132765:	contig of 14498 bp in length
*	132766	132865:	gap of unknown length
*	132866	154092:	contig of 21227 bp in length
*	154093	154192:	gap of unknown length
*	154193	182144:	contig of 27952 bp in length
*	182145	182244:	gap of unknown length
*	182245	212904:	contig of 30660 bp in length

FEATURES	location/Qualifiers
source	1. .212904 /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="4" /clone="RP11-468N14"
BASE COUNT	69110 a 36915 c 37432 g 67121 t 2326 others
ORIGIN	
Query Match	13.1%; Score 362; DB 66; Length 212904;
Best Local Similarity	99.8%; Pred. No. 2.9e+18;
Matches 412; Conservative	0; Mismatches 1; Indels 0; Gaps 0;

OY	1342	ttttaagaagaaatgtaatagaagttaataaagttaacccatgaacaacctgtaaaagccct	1401
Db	34583	TTATTAAGAAGTAAGTGTATGAGATATCAAGAATTACCACTATATCAACCTGTAAAGCCCT	34642
OY	1402	agatcagacagatctctcgtatcgaatctgttcaatgcgccaagaaggacccaagcactgcg	1461
Db	34643	AGATCGACAGACTCTCTGATGTGACTTTGTATGGCCCAAAAGAGGCCAACACCTGGG	34702
OY	1462	atcagctgcaccaatgaacttaacctgtgtccagcaactactatagatgtaattggttccct	1521
Db	34703	ATCACCTGCCCATGACACTACCTGGTGTCCAGACATACCTATATGATGTATGTGGTTCCT	34762
OY	1522	gctgaacctgtgtgcacaactgataatctctgttcaacaanaatgtttttttatcttctgtca	1581
Db	34763	GCTGGCCCTGTGTGGCAACAGCTATATCTCTGTTCACAAATGTTTTTTATTTTCCGTGA	34822
OY	1582	aaattttataaactagaanaagatagaaaaggaggaaatgtaactcttccaattcaagaa	1641
Db	34823	AAAAATTTATAATAAAGCTAGAAACATATGAAAGAGGGGAATATCTTTCCAAATTCAGAA	34882
OY	1642	gacctgaatggagatactccgttaatttccagcacacatagaaattctgttgaanaacctgtcat	1701
Db	34883	GACCTGATATGGGTTATTCCTCGTTAATTTCCAGCCACATAGAAATTTGGTGAAAAACCTTGCTAT	34942

Qy 1702 ttctacattatctatctgttatttattctagctatagcttagaattcca 1754
 Db 34943 TTTCATATATCTATCTGTATTATTATCTACTATATAGCCTAGATTCCA 34995

RESULT 5
 AC055794 138665 bp DNA HTG 06-JUN-2000
 LOCUS Homo sapiens chromosome 4 clone CTD-2005D20 map 4, WORKING DRAFT
 DEFINITION SEQUENCE, 6 unordered pieces.
 AC055794
 AC055794.2 GI:7801441
 HTG: HTGS_PHASE1; HTGS_DRAFT.
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Birren, B., Linton, L., Nusbaum, C. and Lander, E.
 TITLE 1 (bases 1 to 138665)
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 138665)
 AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Abraham, H., Allen, N.,
 Anderson, S., Baldwin, J., Barna, N., Bastien, V., Bede, F.,
 Boguslavsky, L., Boukhgalter, B., Brown, A., Burkett, G.,
 Campopiano, A., Castle, A., Choquet, Y., Colangelo, M., Collins, S.,
 Collamore, A., Cooke, P., Dearrellano, K., Dewar, K., Diaz, J.S.,
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,
 Galagan, J., Gardyna, S., Glade, S., Goyette, M., Graham, L.,
 Grand-Plerre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,
 Howland, J.C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,
 Klein, J., Labrecque, K., Lamazares, R., Landers, J., Lehotzky, J.,
 Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Margulis, N.,
 McCarthy, M., McEwan, P., McCurk, A., McKernan, K., McPheters, R.,
 McElrath, J., Meneus, L., Mihova, T., Miranda, C., Mlenka, V., Morrow, J.,
 Murphy, T., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
 O'Neill, D., Oliver, T.M., Oliver, J., Peterson, K., Pierre, N.,
 Pisanli, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talmes, J.,
 Tesfaye, S., Theodore, J., Tittel, A., Travers, M., Triggillo, J.,
 Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J.,
 Young, G., Zahoun, J., Zimmer, A. and Zody, M.

TITLE
 JOURNAL
 COMMENT
 Submitted (18-APR-2000) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On May 14, 2000 this sequence version replaced g1:7582623.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu

Project Information
 Center project name: L7347
 Center clone name: 2005_D_20

Summary Statistics
 Sequencing vector: M13; M7815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 134168 bases at least Q40
 Consensus quality: 136964 bases at least Q30
 Consensus quality: 137776 bases at least Q20
 Insert size: 17600; agarose-fp
 Insert size: 138165; sum-of-ctnigs
 Quality coverage: 4.1 in Q20 bases; agarose-fp
 Quality coverage: 5.2 in Q20 bases; sum-of-ctnigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 6 ctnigs. The true order of the pieces

* is not known and their order in this sequence record is
 * arbitrary. Gaps between the ctnigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.
 * 1 4325: contig of 4325 bp in length
 * 4326 4425: gap of 100 bp
 * 4426 14722: contig of 10297 bp in length
 * 14723 14822: gap of 100 bp
 * 14823 30375: contig of 15553 bp in length
 * 30376 30475: gap of 100 bp
 * 30476 57367: contig of 26892 bp in length
 * 57368 57467: gap of 100 bp
 * 57468 95400: contig of 37933 bp in length
 * 95401 95500: gap of 100 bp
 * 95501 138665: contig of 43165 bp in length.
 Location/Qualifiers
 1. 138665
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /map="4"
 /chromosome="4"
 /clone="CTD-2005D20"
 /clone.lib="CTD Human BAC"
 1. 4325
 /note="assembly-fragment"
 misc_feature 4426..14722
 /note="assembly-fragment"
 misc_feature 14823..30375
 /note="assembly-fragment"
 misc_feature 30476..57367
 /note="assembly-fragment"
 misc_feature 57468..95400
 /note="assembly-fragment"
 misc_feature 95501..138665
 /note="assembly-fragment"
 BASE COUNT 45118 a 24794 c 24580 g 43671 t
 ORIGIN

Query Match 2.6%; Score 72; DB 72; Length 138665;
 Best Local Similarity 100.0%; Pred. No. 8.9e+28;
 Matches 72; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2071 ttttcaatttaataagcccttctacataccagcatatgattctgacaaagaatt 2130
 Db 97061 TTTTTCATTTAAATTAAGCCCTTCAATACACGACATTCATCTCAGACATGAATT 97120
 Qy 2131 gctaaatgac 2142
 Db 97121 GCTAAATGAC 97132

RESULT 6
 HSA6054 1766 bp mRNA PRI 16-JUL-1999
 LOCUS Homo sapiens mRNA for UDP glucuronosyltransferase.
 DEFINITION AJ006054
 ACCESSION AJ006054.1 GI:4753765
 VERSION UDP glucuronosyltransferase; ugt2A1 gene.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 AUTHORS Jedlitschky, G., Cassidy, A.J., Sales, M., Pratt, N. and Burchell, B.
 TITLE Cloning and characterization of a novel human olfactory
 UDP-glucuronosyltransferase
 JOURNAL Biochem. J. 340 (Pt 3), 837-843 (1999)
 MEDLINE 99289328
 REFERENCE 2 (bases 1 to 1766)
 AUTHORS Cassidy, A.J.

TITLE Direct Submission
JOURNAL Submitted (07-MAY-1998) Cassidy A.J., Molecular and Cellular Pathology, University of Dundee, University Dept. of Molecular and Cellular Pathology, Ninewells Hospital, Dundee, DD1 9ST, SCOTLAND

FEATURES
 source
 1. .1666
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /rname="factory"
 64. .1647
 /gene="ugt2a1"
 64. .1647
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 /EC_number="2.4.1.17"
 /codon_start=1
 /product="UDP glucuronosyltransferase"
 /protein_id="CAB41974.1"
 /db_xref="GI:4753766"
 /translation="MLNLLFLSLQISLIGTTLGCVNLIMPMEGSHMLNKKIITDELI
 KKEHNVAVASGALFETPTSPSTFEIKVPKKEIEGVKIDVSTWLEMRPSPS
 TIMRFQEMAKYIKDFHMYSOEICDGLKNOOLMKLKSKEFVYVSDVPFGCDIVA
 ILGIDPMYSLNFSRSPASTYERKCKRYPSPYPAVLSELTQDMSTDIRNFISHL
 QDYFETLMSWDSITSKALGRPTTCTETWGAELMLRTWDFEPRPYLDPFEFVG
 GLCKRPAPLPEKMEEFIQSGKNGVVSLSGMYKNLTKERANLTAOLAQIPKYL
 WYKGRKPAITLNNITQLEFDIMIPONDILGHKTKAFTTGGTNGIYAIHGVMPVGP
 MPADDPNTAHMKAKGAAYEVNLTMTSYDLISALRTYINPESYKENARLSRIHDD
 PKRPLDRAVFMIEFVMRHKKAKHLRYAANDLWFOYHSLDIVGIFLLVCYTTAIFLYIO
 CCLFSGCKRGKIGKKRR"

BASE COUNT 542 a 359 c 363 g 502 t

ORIGIN

Query Match 2.0%; Score 56; DB 93; Length 1766;
 Best Local Similarity 100.0%; Pred.No.3.8e-19;
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1403 gacgagcagctcttcgacgagctgtgtcatcgccacaaagagcagcact 1458
 |||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1429 GATCGAGCATCTTCTCGATCGAGTTGTGTCATGCCACAAAGAGCCACACT 1484

RESULT 7
AC011254 169246 bp DNA HTG 26-MAY-2000
LOCUS Homo sapiens chromosome 4 clone RP11-401E5 map 4, WORKING DRAFT
DEFINITION SEQUENCE, 12 unordered pieces.
AC011254 AC011254.3 GI:7107765
VERSION HTG; HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 169246)
AUTHORS Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
 Balmain, A., Castle, A., Colangelo, M., Collins, S., Collins, A.,
 Cooke, P., DeRubeis, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
 Ferreira, P., Fitzhugh, W., Forrest, C., Funk, R., Gage, D.,
 Galagan, J., Gardy, S., Grant, G., Hargreaves, B., Heath, A., Horton, L.,
 Howland, J., Johnson, R., Jones, C., Kann, L., Karas, A., Klein, J.,
 Lehotzky, J., Lien, C., Locke, K., MacDonald, P., Margolis, N.,
 McKernan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
 Morrow, J., Naylor, J., Norman, C. H., O'Connor, F., O'Donnell, P.,
 Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
 Tene, S., Tinsley, A., Vassiliev, N., Vo, A., Wheeler, J., Wu, X.,
 Wyman, D., Ye, W. J., Zimmer, A. and Zody, M.
JOURNAL Direct Submission

JOURNAL Submitted (05-OCT-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
COMMENT On Feb 28, 2000 this sequence version replaced gi:6094610.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Center: Whitehead Institute/MIT Center for Genome Research
Genome Center
Center code: WIMR
Web site: http://www.seq.wi.mit.edu/
Contact: sequence_submissions@genome.wi.mit.edu
Project information
Center project name: L1759
Center clone name: 401_E5

Summary Statistics
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: Dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.960731
 Consensus quality: 129285 bases at least Q40
 Consensus quality: 148859 bases at least Q30
 Consensus quality: 160948 bases at least Q20
 Insert size: 172000; agarose-fp
 Insert size: 168146; sum-of-consigs
 Quality coverage: 3.4 in Q20 bases; sum-of-consigs
 Quality coverage: 3.5 in Q20 bases; sum-of-consigs

NOTE: This is a 'working draft' sequence. It currently
 consists of 12 contigs. The true order of the pieces
 is not known and their order in this sequence record is
 arbitrary. Gaps between the contigs are represented as
 runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 as soon as it is available and the accession number will
 be preserved.

1 2121: contig of 2121 bp in length
 2122 2221: gap of 100 bp
 2222 5198: contig of 2977 bp in length
 5199 5298: gap of 100 bp
 5299 10736: contig of 5438 bp in length
 10737 10836: gap of 100 bp
 10837 19995: contig of 9159 bp in length
 19996 20095: gap of 100 bp
 20096 29257: contig of 9162 bp in length
 29258 29357: gap of 100 bp
 29358 43227: contig of 13870 bp in length
 43228 43327: gap of 100 bp
 43328 53743: contig of 10416 bp in length
 53744 53843: gap of 100 bp
 53844 64325: contig of 10482 bp in length
 64326 64425: gap of 100 bp
 64426 83384: contig of 18959 bp in length
 83385 83484: gap of 100 bp
 83485 109710: contig of 26226 bp in length
 109711 109810: gap of 100 bp
 109811 134388: contig of 24578 bp in length
 134389 134488: gap of 100 bp
 134489 169246: contig of 34758 bp in length.

FEATURES
source
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 /db_xref="taxon:9606"
 /chromosome="4"
 /map="4"
 /clone="RP11-401E5"
 /clone_lib="RP11 Human Mat: BAC"
 1. .2121
 /note="assembly-fragment"
 2222. .5198
 /note="assembly-fragment"
 5299. .10736
 /note="assembly-fragment"
 10837. .19995
 /note="assembly-fragment"

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misc_feature      20096..29257
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misc_feature      29358..43227
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misc_feature      43328..53743
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                   vector_side:right"
misc_feature      53844..64325
                   /note="assembly_fragment"
misc_feature      64426..83384
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misc_feature      83485..109710
                   /note="assembly_fragment"
misc_feature      109811..134388
                   /note="assembly_fragment"
misc_feature      134489..169246
                   /note="assembly_fragment"
                   clone_end:SP6
                   vector_side:right"
BASE COUNT      52651 a 30209 c 30094 g 55185 t 1107 others
ORIGIN
Query Match      2.0%; Score 56; DB 62; Length 169246;
Best Local Similarity 100.0%; Pred. No. 6.3e-19;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1403 gatcgagcagctctctgcatcgattgcatgcacacaaagagccagacact 1458
    |||||||
Db 16890 GATCGAGCAGCTCTTGTGATCGATTGTGCATGCGCCACAAGGACCAAGCAGCAGCCT 16945

RESULT 8
LOCUS      HUM4STS886/c      386 bp      DNA      STS      17-AUG-1993
DEFINITION      Human Chromosome 4 (clone p4-1075) STS4-886, sequence tagged site.
ACCESSION      L09985
VERSION      L09985.1 GI:177711
KEYWORDS      STS; primer; sequence tagged site.
SOURCE      Homo sapiens
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 386)
Goodall,R.D., disibio,G., Xu,H., Lang,D.B., Daddgar,J., Magrane,G.,
Dugalczyk,A., Smith,K.A., Cox,D.R., Masters,S.B. and Myers,R.M.
The development of sequence-tagged sites for human chromosome 4
Hum. Mol. Genet. 2, 1271-1288 (1993)
94004872
Submitted by: Human Genome Mapping Center,
University of California San Francisco, Box 0925,
San Francisco, CA 94143-0925, USA
e-mail: hgmcp@obscfql.ucsf.edu
Primer A: CATTAATCTCTTATTAAGTACCTC
Primer B: TGCTCTGATGATGAATAAGTACCTC
PCR components: 25 ng of human genomic DNA, 10 pmol of each
Oligonucleotide,
200 micro-M dNTPs, 0.25 U Tsg polymerase (Cetus) in 10 micro-l of
50 mM KCl-20 mM Tris-HCl, pH 8.3 (at room temp), 2.5 mM MgCl-2.
Thermocycler: PE 9600
PCR Profile: Initial denaturation: 94 degrees C for 1.5
minutes
Denaturation: 62 degrees C for 15 seconds Annealing:
72 degrees C for 3.5 minutes PCR cycles: 30
Final extension: 72 degrees C for 3.5 minutes.
Location/Qualifiers
FEATURES
source      1..386
              /organism="Homo sapiens"
              /db_xref="taxon:9606"
STS      103..295
primer_bind      103..130

```

```

Primer_bind      complement(271..295)
BASE COUNT      134 a 51 c 54 g 144 t 3 others
ORIGIN
Query Match      1.8%; Score 50; DB 54; Length 386;
Best Local Similarity 100.0%; Pred. No. 6.7e-16;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 2153 tacactcagaatagttgtctatattccacataccctccatgcat 2202
    |||||||
Db 385 TACACTCAGAAATAGTTGTCTATATTCCACATACCTCATTAATGTCAT 336

RESULT 9
AC012582      138232 bp      DNA      HTG      01-JUN-2000
LOCUS      Homo sapiens clone Rp11-3C24, *** SEQUENCING IN PROGRESS ***, 53
DEFINITION      Unordered pieces.
ACCESSION      AC012582
VERSION      AC012582.4 GI:8137462
KEYWORDS      HTG; HTGS_PHASE1.
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
1 (bases 1 to 138232)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
Homo sapiens, clone Rp11-3C24
Unpublished
2 (bases 1 to 138232)
Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
Baldwin,D., Barna,N., Beckert,R., Boguslavsky,L., Boukhalter,B.,
Brown,A., Castle,A., Collins,S., Collins,S., Collins,S., Collins,S.,
Cooke,P., DeRellano,K., Dewar,K., Domingo,M., Donelan,L., Doyle,M.,
Ferreira,P., Fitzhugh,W., Forrest,C., Funke,R., Gage,D.,
Gallagan,J., Gairyna,S., Grant,G., Hays,B., Heaford,A., Horton,L.,
Howland,J.C., Johnson,R., Jones,C., Karm,L., Karkas,A., Klein,J.,
Lehoczky,J., Lieu,C., Locke,K., MacDonald,P., Marquis,N.,
McEwan,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
Morrow,J., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,
Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severy,P.,
Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
Teafaye,S., Tittell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
Direct Submission
Submitted (30-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Jun 1, 2000 this sequence version replaced gi:7107861.
All repeats were identified using RepeatMasker:
http://ftp.genome.washington.edu/RM/RepeatMasker.html
Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
Project Information
Center project name: 3_C_24

```

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 53 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

* 1 1640: contig of 1640 bp in length
 * 1641 1740: gap of 100 bp
 * 1741 2943: contig of 1203 bp in length
 * 2944 3043: gap of 100 bp


```
* 3044 4897: contig of 1854 bp in length
* 4898 4997: gap of 100 bp
* 4998 6114: contig of 1117 bp in length
* 6115 6214: gap of 100 bp
* 6215 7665: contig of 1451 bp in length
* 7666 7765: gap of 100 bp
* 7766 9188: contig of 1423 bp in length
* 9189 9288: gap of 100 bp
* 9289 11371: contig of 2083 bp in length
* 11372 11471: gap of 100 bp
* 11472 13194: contig of 1723 bp in length
* 13195 13294: gap of 100 bp
* 13295 14324: contig of 1030 bp in length
* 14325 14424: gap of 100 bp
* 14425 15511: contig of 1087 bp in length
* 15512 15611: gap of 100 bp
* 15612 17362: contig of 1751 bp in length
* 17363 17462: gap of 100 bp
* 17463 19182: contig of 1720 bp in length
* 19183 19282: gap of 100 bp
* 19283 20717: contig of 1435 bp in length
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* 35134 35233: gap of 100 bp
* 35234 37156: contig of 1923 bp in length
* 37157 37256: gap of 100 bp
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* 79941 80040: gap of 100 bp
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* 83641 83740: gap of 100 bp
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* 94260 94359: gap of 100 bp
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* 96911 97010: gap of 100 bp
* 97011 100209: contig of 3199 bp in length
* 100210 100309: gap of 100 bp
* 100310 105003: contig of 4694 bp in length
* 105004 105103: gap of 100 bp
* 105104 110031: contig of 4928 bp in length
* 110032 110131: gap of 100 bp
* 110132 115352: contig of 5221 bp in length
* 115353 115452: gap of 100 bp
* 115453 120961: contig of 5509 bp in length
* 120962 121061: gap of 100 bp
* 121062 126155: contig of 5094 bp in length
* 126156 126255: gap of 100 bp
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Best local Similarity 100.0%; Pred. No. 2.1e-08;

Matches 37: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1124 catcccaaaacgaagcttctactcatgttgaa 1160
 DB 110344 CATCCCAAAACCAAGCTTTATCACTCATGTGGA 110380

RESULT 10
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 ACCESSION AC013296.5 GI:9121251
 VERSION AC013296.5
 KEYWORDS HTG; HTGS_PHASE0.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 226077)
 Birren,B., Linton,L., Nusbaum,C. and Lander,E.
 Unpublished
 2 (bases 1 to 226077)
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,M.,
 Baldwin,J., Barna,N., Beckert,R., Boguslavsky,L., Boukhalter,B.,
 Brown,A., Castle,A., Colangelo,M., Collins,S., Collymore,A.,
 Cooke,P., Deavrellano,K., Dewar,K., Domino,M., Donelan,L., Doyle,M.,
 Feltre,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D.,
 Galagan,J., Gardyna,S., Grant,G., Hagos,B., Heaford,A., Horton,L.,
 Howland,J.C., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J.,
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 Morrow,P., McGurk,A., McKernan,K., McLaughlin,J., Meldrum,J.,
 Peterson,K., Pollara,V., Riley,R., Roy,A., Santos,R., Severi,P.,
 Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J.,
 Teste,S., Tirrell,A., Vassiliev,H., Vo,A., Wheeler,J., Wu,X.,
 Wyman,D., Ye,W.J., Zimmer,A. and Zody,M.
 Direct Submission
 Submitted (06-NOV-1999) Whitehead Institute/MIT Center for Genome
 Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Jul 13, 2000 this sequence version replaced gi:6514003.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIBR
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 Project Information
 Center project name: L2775
 Center clone name: 3_M18

NOTE: This record contains 246 individual
 * sequencing reads that have not been assembled into
 * contigs. Runs of N are used to separate the reads
 * and the order in which they appear is completely
 * arbitrary. Low-pass sequence sampling is useful for
 * identifying clones that may be gene-rich and allows
 * overlap relationships among clones to be deduced.
 * However, it should not be assumed that this clone
 * will be sequenced to completion. In the event that
 * the record is updated, the accession number will
 * be preserved.

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Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION Human UDP glucuronosyltransferase precursor (UGT2B15) mRNA, complete cds.
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VERSION U08854.1 GI:475758
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2090)
Green, M.D., Ojura, E.M., and Tepfly, T.R.
TITLE Stable expression of a human liver UDP-glucuronosyltransferase (UGT2B15) with activity toward steroid and xenobiotic substrates
JOURNAL Drug Metab. Dispos. 22 (5), 799-805 (1994)
MEDLINE 95136867
REFERENCE 2 (bases 1 to 2090)
Green, M.D.
AUTHORS
TITLE Direct Submission
JOURNAL Submitted (13-APR-1994) Mitchell D. Green, Department of Pharmacology, The University of Iowa, Iowa City, IA 52242, USA
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Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1417 GAGTTGTCATCGCCACAAAGAGCAAGCACCCT 1453

RESULT 12
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DEFINITION Homo sapiens UDP-glucuronosyltransferase 2B15 (UGT2B15) mRNA,

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
99063792
2 (bases 1 to 181117)
Meyer, R., Drone, K., Hawkins, M. and McDill, B.
The sequence of Homo sapiens BAC clone RP11-185H6
Unpublished
3 (bases 1 to 181117)
Waterston, R.H.
Direct Submission
Submitted (30-DEC-1999) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
4 (bases 1 to 181117)
Waterston, R.
Direct Submission
Submitted (08-NOV-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 8, 2000 this sequence version replaced gi:7630882.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapiens@watson.wustl.edu
----- Summary Statistics
Center project name: H_NH0185H06

NOTICE: This sequence may not represent the entire insert of this
clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
McPherson, Department of Genetics, Washington University, St. Louis
MO. For additional information about the map position of this
sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:
The RPCI-11 human BAC library was made from the blood of one male
donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Feinguen, E.,
Tateno, M., Catanesi, J.J. and de Jong, P.J. (1998) An improved
approach for construction of bacterial artificial chromosome
libraries. Genomics 51:1-8. The clone may be obtained either from
Research Genetics, Inc. (<http://www.resgen.com>) or Pletier de Jong
and coworkers at the Roswell Park Cancer Institute
(<http://bacpac.med.buffalo.edu>)
VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is CTD-2005D20. Actual start of
this clone is at base position 1 of RP11-185H6; actual end is at
base position 18117 of RP11-185H6.

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271. 444
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DB 109805 GAGTTGTCTATGCCCAAAAGGACCAAGCACCT 109839

RESULT 15

AF072223 2075 bp mRNA PRI 22-JAN-1999
LOCUS AF072223
DEFINITION Macaca fascicularis UDP-glucuronosyltransferase mRNA, complete cds.
ACCESSION AF072223
VERSION AF072223.1 GI:3273888
KEYWORDS
SOURCE crab-eating macaque.
ORGANISM Macaca fascicularis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecinae; Macaca.
REFERENCE
1 (bases 1 to 2075)
Barbier, O., Belanger, A. and Hum, D.W.
Cloning and characterization of a simian
UDP-glucuronosyltransferase enzyme UGT2B20, a novel C19
steroid-conjugating protein

JOURNAL Biochem. J. 337 (Pt 3), 567-574 (1999);
MEDLINE 99112924
REFERENCE 2 (bases 1 to 2075)
AUTHORS Barbier, O., Belanger, A. and Hum, D.W.
TITLE Direct Submission
JOURNAL Submitted (15-JUN-1998) Laboratory of Molecular Endocrinology, CHUL
Research Center, Boulevard Laurier 2705, Quebec, Que G1V 4G2,
Canada

FEATURES
Source Location/Qualifiers
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DB 1100 CTCTGTGTCATCCCAAAAGCCTTTAT 1131

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